

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/593,672
Source: IFWP
Date Processed by STIC: 9/29/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/29/2006

PATENT APPLICATION: US/10/593,672

TIME: 11:06:50

Input Set : F:\11281-118-999 - seqlist (final).txt

Output Set: N:\CRF4\09292006\J593672.raw

3 <110> APPLICANT: Neurotech Pharmaceuticals Co., Ltd.
 4 Han, Pyung Lim
 5 Lee, Kang-Woo
 6 Yang, Sung-Don
 7 Song, Jin-Sook
 9 <120> TITLE OF INVENTION: TRANSGENIC MICE INDUCING ALZHEIMER'S
 10 DISEASE EXPRESSING MUTANT BETACTF99
 13 <130> FILE REFERENCE: 11281-118-999
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/593,672
 16 <141> CURRENT FILING DATE: 2006-09-20
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 19 <151> PRIOR FILING DATE: 2004-04-01
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 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 26 <211> LENGTH: 3148
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
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 33 cgcgatgctg cccggttttg cactgtctct gctggccgcc tggacggctc gggcgctgga 180
 34 ggtacccact gatggtaatg ctggcctgct ggctgaacct cagattgcca tgttctgtgg 240
 35 cagactgaac atgcacatga atgtccagaa tgggaagtgg gattcagatc catcaggga 300
 36 caaacctgc attgatacca aggaaggcat cctgcagtat tgccaagaag tctacctga 360
 37 actgcagatc accaatgtgg tagaagccaa ccaaccagt accatccaga actggtgcaa 420
 38 gcggggccgc aagcagtgc agacccatcc ccactttgtg attccctacc gctgcttagt 480
 39 tggtagtgg gtaagtgat cccttctcgt tctgacaag tgcaaattct tacaccagga 540
 40 gaggatggat gtttgcaaaa ctcacttca ctggcacacc gtcgcaaag agacatgcag 600
 41 tgagaagagt accaacttgc atgactacgg catgttgctg cctgcgga ttgacaagt 660
 42 ccgaggggta gagtttgtgt gttgccact ggctgaagaa agtgacaatg tggattctgc 720
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 45 agaagaagcc gatgatgacg aggacgatga ggatggtgat gaggtagagg aagaggctga 900
 46 ggaaccctac gaagaagcca cagagagaac caccagcatt gccaccacca ccaccaccac 960
 47 cacagagtct gtggaagagg tggttcgaga ggtgtgctct gaacaagccg agacggggcc 1020
 48 gtgccgagca atgatctccc gctggtactt tgatgtgact gaagggaagt gtgccccatt 1080
 49 cttttacggc ggatgtggcg gcaaccggaa caactttgac acagaagagt actgcatggc 1140
 50 cgtgtgtggc agcgccattc ctacaacagc agccagtacc cctgatgccg ttgacaagta 1200
 51 tctcgagaca cctggggatg agaatgaaca tgccatttc cagaaagcca aagagaggct 1260
 52 tgaggccaag caccgagaga gaatgtccca ggtcatgaga gaatgggaag aggcagaacg 1320
 53 tcaagcaaag aacttgccca aagctgataa gaaggcagtt atccagcatt tccaggagaa 1380
 54 agtggaaatc ttggaacagg aagcagccaa cgagagacag cagctggtgg agacacacat 1440

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56 cgctctgcag gctgttccctc ctccggcctcg tcacgtgttc aatatgctaa agaagtatgt 1560
57 ccgcgccagaa cagaaggaca gacagcacac cctaaagcat ttcgagcatg tgcgcatggg 1620
58 ggatcccaag aaagccgctc agatccgggc ccaggttatg acacacctcc gtgtgattta 1680
59 tgagcgcgat aatcagtcctc tctccctgct ctacaacgtg cctgcagtgg ccgaggagat 1740
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61 caacatgatt agtgaaccaa ggatcagtta cggaaacgat gctctcatgc catctttgac 1860
62 cgaaacgaaa accaccgtgg agctccttcc cgtgaatgga gagttcagcc tggacgatct 1920
63 ccagccgtgg cattcttttg gggctgactc tgtgccagcc aacacagaaa acgaagttga 1980
64 gctgttgat gcccgccctg ctgccgaccg aggactgacc actcgaccag gttctgggtt 2040
65 gacaaatata aagacggagg agatctctga agtgaagatg gatgcagaat tccgacatga 2100
66 ctgaggatat gaagttcatc atcaaaaatt ggtgttcttt gcagaagatg tgggttcaaa 2160
67 caaaggtgca atcattggac tcatggtggg cgggtgtgtc atagcgacag tgatcgcat 2220
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69 tgacgccgct gtcaccccag aggagcgcca cctgtccaag atgcagcaga acggctacga 2340
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71 tgaagttgga cagcaaaacc attgcttcac taccatcgg tgtccattta tagaataatg 2460
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74 tttacatttt ggtctctata ctacattatt aatgggtttt gtgtactgta aagaatttag 2640
75 ctgtatcaaa ctagtgcag aatagattct ctccgtatta tttatcacat agccccttag 2700
76 ccagttgtat attattcttg tggtttgtga cccaattaa tccacttta catatgcttt 2760
77 aagaatcgat ggggggatgt tcatgtgaac gtgggagttc agctgcttct cttgcctaag 2820
78 tattcctttc ctgatcacta tgcattttta agttaaacat ttttaagat ttcagatgct 2880
79 ttagagagat tttttttcca tgactgcatt ttactgtaca gattgctgct tctgctatat 2940
80 ttgtgatata ggaattaaga ggatacacac gtttgtttct tcgtgcctgt tttatgtgca 3000
81 cacattaggg attgagactt caagcttttc tttttttgtc cacgtatctt tgggtctttg 3060
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 751

87 <212> TYPE: PRT

88 <213> ORGANISM: Homo sapiens

90 <400> SEQUENCE: 2

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93 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
94 20 25 30
95 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
96 35 40 45
97 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
98 50 55 60
99 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
100 65 70 75 80
101 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
102 85 90 95
103 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
104 100 105 110
105 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu

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108	130							135				140				
109	Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
110	145							150				155				
111	Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
112				165								170				
113	Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
114				180								185				
115	Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
116	195							200				205				
117	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
118	210							215				220				
119	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	Glu
120	225							230				235				
121	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
122				245								250				
123	Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
124				260								265				
125	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
126	275							280				285				
127	Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
128	290							295				300				
129	Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
130	305							310				315				
131	Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
132				325								330				
133	Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Ile	Pro	Thr	Thr	Ala	Ala	Ser	Thr
134				340								345				
135	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu
136	355							360				365				
137	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg
138	370							375				380				
139	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln
140	385							390				395				
141	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	Gln	His	Phe
142				405								410				
143	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln
144				420								425				
145	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp
146	435							440				445				
147	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val
148	450							455				460				
149	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg
150	465							470				475				
151	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	Glu	His	Val
152				485								490				
153	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met
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155 Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
156          515          520          525
157 Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
158          530          535          540
159 Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
160 545          550          555          560
161 Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
162          565          570          575
163 Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
164          580          585          590
165 Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
166          595          600          605
167 Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
168          610          615          620
169 Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
170 625          630          635          640
171 Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
172          645          650          655
173 Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
174          660          665          670
175 Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
176          675          680          685
177 Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
178          690          695          700
179 Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
180 705          710          715          720
181 Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
182          725          730          735
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188 <211> LENGTH: 2256
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: C-terminal fragment of APP bearing V717F mutation
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197 cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
198 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
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201 ggccgcaagc agtgcaagac ccacccccac tttgtgattc cctaccgctg cttagtgtgt 360
202 gagtttgtaa gtgatgccct tctcgttctt gacaagtgca aattcttaca ccaggagagg 420
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206 gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg 660
207 agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720

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210 gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900
211 cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960
212 tacggcggat gtggcggaac ccggaacaac ttgacacag aagagtactg catggccgtg 1020
213 tgtggcagcg ccattcctac aacagcagcc agtaccctg atgccgttga caagtatctc 1080
214 gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140
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221 cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag 1560
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227 gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccaggttc tgggttgaca 1920
228 aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980
229 ggatataaga ttcatacatc aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040
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231 ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac 2160
232 gccgtgttca cccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat 2220
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235 <210> SEQ ID NO: 4

236 <211> LENGTH: 770

237 <212> TYPE: PRT

238 <213> ORGANISM: Homo sapiens

240 <400> SEQUENCE: 4

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244 20 25 30
245 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
246 35 40 45
247 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
248 50 55 60
249 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
250 65 70 75 80
251 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
252 85 90 95
253 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
254 100 105 110
255 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
256 115 120 125
257 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number